

# SEQUENCE PROTOCOL

<110> Degussa AG

<120> Nucleotide sequences which code for the ppgK gene

<130> 000569 BT

<140>

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<170> PatentIn Ver. 2.1

<210> 1

<211> 1239

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (237)..(1022)

<223> ppgK gene

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cgcttatccc tgatacgtac agcggtaagc gtggcagttt ccgcggcgat ggcaacgcaac 180
tcattaaacg attgttggtc cataagacca tcatcggtgt ttttttagaa aattgc ctg 239
Met
1

cca aaa gcc gaa gta att tgt aca ctt ggg cgc atg act gag act gga 287
Pro Lys Ala Glu Val Ile Cys Thr Leu Gly Arg Met Thr Glu Thr Gly
5 10 15

ttt gga att gat atc ggt ggc tcc ggc atc aaa ggc gcc cgc gtt aac 335
Phe Gly Ile Asp Ile Gly Gly Ser Gly Ile Lys Gly Ala Arg Val Asn
20 25 30

ctt aag acc ggt gag ttt att gat gaa cgc ata aaa atc gcc acc cct 383
Leu Lys Thr Gly Glu Phe Ile Asp Glu Arg Ile Lys Ile Ala Thr Pro
35 40 45

aag cca gca acc cca gag gct gtc gcc gaa gta gtc gca gag att att 431
Lys Pro Ala Thr Pro Glu Ala Val Ala Glu Val Val Ala Glu Ile Ile
50 55 60 65

tct caa gcc gaa tgg gag ggt ccg gtc gga att acc ctg ccg tcg gtc 479
Ser Gln Ala Glu Trp Glu Gly Pro Val Gly Ile Thr Leu Pro Ser Val
70 75 80

gtt cgc ggg cag atc gcg cta tcc gca gcc aac att gac aag tcc tgg 527
Val Arg Gly Gln Ile Ala Leu Ser Ala Ala Asn Ile Asp Lys Ser Trp
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atc ggc acc gat gtg cac gaa ctt ttt gac cgc cac cta aat ggc cga 575
Ile Gly Thr Asp Val His Glu Leu Phe Asp Arg His Leu Asn Gly Arg
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gag atc acc gtt ctc aat gac gca gac gcc gcc ggc atc gcc gaa gca 623
Glu Ile Thr Val Leu Asn Asp Ala Asp Ala Ala Gly Ile Ala Glu Ala
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acc ttt ggc aac cct gcc gca cgc gaa ggc gca gtc atc ctg ctg acc 671
Thr Phe Gly Asn Pro Ala Ala Arg Glu Gly Ala Val Ile Leu Leu Thr
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ctt ggt aca ggt att gga tcc gca ttc ctt gtg gat ggc caa ctg ttc 719
Leu Gly Thr Gly Ile Gly Ser Ala Phe Leu Val Asp Gly Gln Leu Phe
      150                      155                      160

ccc aac aca gaa ctc ggt cac atg atc gtt gac ggc gag gaa gca gaa 767
Pro Asn Thr Glu Leu Gly His Met Ile Val Asp Gly Glu Glu Ala Glu
      165                      170                      175

cac ctt gca gca gca tcc gtc aaa gaa aac gaa gat ctg tca tgg aag 815
His Leu Ala Ala Ala Ser Val Lys Glu Asn Glu Asp Leu Ser Trp Lys
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aaa tgg gcg aag cac ctg aac aag gtg ctg agc gaa tac gag aaa ctt 863
Lys Trp Ala Lys His Leu Asn Lys Val Leu Ser Glu Tyr Glu Lys Leu
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Phe Ser Pro Ser Val Phe Ile Ile Gly Gly Gly Ile Ser Arg Lys His
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gaa aag tgg ctt cca ttg atg gag cta gac act gac att gtc cca gct 959
Glu Lys Trp Leu Pro Leu Met Glu Leu Asp Thr Asp Ile Val Pro Ala
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Gln His Leu Thr Pro
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tataatggaa cgctgatcgt ggacaagagt taaccatgag attgattcac ccctttaagc 1182

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<213> Corynebacterium glutamicum

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Arg	Glu	Ile	Thr	Val	Leu	Asn	Asp	Ala	Asp	Ala	Ala	Gly	Ile	Ala	Glu	115	120	125	
Ala	Thr	Phe	Gly	Asn	Pro	Ala	Ala	Arg	Glu	Gly	Ala	Val	Ile	Leu	Leu	130	135	140	
Thr	Leu	Gly	Thr	Gly	Ile	Gly	Ser	Ala	Phe	Leu	Val	Asp	Gly	Gln	Leu	145	150	155	160
Phe	Pro	Asn	Thr	Glu	Leu	Gly	His	Met	Ile	Val	Asp	Gly	Glu	Glu	Ala	165	170	175	
Glu	His	Leu	Ala	Ala	Ala	Ser	Val	Lys	Glu	Asn	Glu	Asp	Leu	Ser	Trp	180	185	190	
Lys	Lys	Trp	Ala	Lys	His	Leu	Asn	Lys	Val	Leu	Ser	Glu	Tyr	Glu	Lys	195	200	205	
Leu	Phe	Ser	Pro	Ser	Val	Phe	Ile	Ile	Gly	Gly	Gly	Ile	Ser	Arg	Lys	210	215	220	
His	Glu	Lys	Trp	Leu	Pro	Leu	Met	Glu	Leu	Asp	Thr	Asp	Ile	Val	Pro	225	230	235	240
Ala	Glu	Leu	Arg	Asn	Arg	Ala	Gly	Ile	Val	Gly	Ala	Ala	Met	Ala	Val	245	250	255	
Asn	Gln	His	Leu	Thr	Pro	260													